

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 31, 2001, 10:44:38 ; Search time 1165.71 Seconds  
(without alignments)  
3990.731 Million cell updates/sec

Title: US-09-424-705-1  
Perfect score: 909  
Sequence: 1 gaattcataaagagagagaa.....atcacatcataatctaga 909

Scoring table: IDENTITY\_NDC  
Gapop 10.0 , Gapext 1.0

Searched: 118133 seqs, 2558875100 residues  
2236266

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl: \*  
1: gb\_ba1: \*  
2: gb\_ba2: \*  
3: gb\_cm: \*  
4: gb\_ov: \*  
5: gb\_ph: \*  
6: gb\_pl1: \*  
7: gb\_pl2: \*  
8: gb\_pr1: \*  
9: gb\_pr2: \*  
10: gb\_pr3: \*  
11: gb\_ro: \*  
12: gb\_sy: \*  
13: gb\_un: \*  
14: em\_fun: \*  
15: em\_hum1: \*  
16: em\_hum2: \*  
17: em\_in: \*  
18: em\_com: \*  
19: em\_or: \*  
20: em\_ov: \*  
21: em\_pat: \*  
22: em\_ph: \*  
23: em\_pl: \*  
24: em\_ro: \*  
25: em\_sts: \*  
26: em\_sy: \*  
27: em\_un: \*  
28: em\_vi: \*  
29: gb\_ba3: \*  
30: gb\_in1: \*  
31: gb\_in2: \*  
32: gb\_in3: \*  
33: gb\_pl3: \*  
34: gb\_pr4: \*  
35: em\_ba1: \*  
36: em\_ba2: \*  
37: em\_htg1: \*  
38: em\_htg2: \*  
39: em\_htg3: \*  
40: em\_htg4: \*  
41: em\_htg5: \*  
42: em\_htg6: \*  
43: em\_htg7: \*

44: em\_htg8: \*  
45: em\_htg9: \*  
46: em\_htg10: \*  
47: em\_hum3: \*  
48: em\_hum4: \*  
49: em\_hum5: \*  
50: em\_hum6: \*  
51: gb\_pr5: \*  
52: gb\_pr6: \*  
53: gb\_pr7: \*  
54: gb\_htg1: \*  
55: gb\_htg2: \*  
56: gb\_htg3: \*  
57: gb\_htg4: \*  
58: gb\_htg5: \*  
59: gb\_htg6: \*  
60: gb\_htg7: \*  
61: gb\_htg8: \*  
62: gb\_htg9: \*  
63: gb\_htg10: \*  
64: gb\_htg11: \*  
65: gb\_htg12: \*  
66: gb\_htg13: \*  
67: gb\_htg14: \*  
68: gb\_htg15: \*  
69: gb\_htg16: \*  
70: gb\_htg17: \*  
71: gb\_htg18: \*  
72: gb\_htg19: \*  
73: gb\_htg20: \*  
74: gb\_htg21: \*  
75: gb\_htg22: \*  
76: gb\_htg23: \*  
77: gb\_sts1: \*  
78: gb\_sts2: \*  
79: gb\_vil: \*  
80: gb\_vil2: \*  
81: gb\_pat1: \*  
82: gb\_pat2: \*  
83: em\_htg0: \*  
84: gb\_htg24: \*  
85: gb\_pr8: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	625.4	68.8	1653	13 AX011208	AX011208 Sequence
2	622.6	68.5	1698	13 AX011206	AX011206 Sequence
3	613.4	67.5	1611	51 AX014270	AX014270 Sequence
4	569	62.6	3991	12 ASY12778	Y12778 Artificial
5	527.4	58.0	1797	82 I84705	I84705 Sequence 2
6	515.2	56.7	810	81 A45006	A45006 Sequence 1
7	504	55.4	738	11 AF074900	AF074900 Mus muscu
8	499.8	55.0	717	11 AF025535	AF025535 Mus muscu
9	496	54.6	723	11 AF035617	AF035617 Mus muscu
10	490	53.9	1815	12 AF189283	AF189283 Synthetic
11	489.8	53.9	735	12 AF162710	AF162710 Synthetic
12	489	53.8	843	81 A83223	A83223 Sequence 43
13	488.6	53.8	1254	12 AF148718	AF148718 Synthetic
14	487.6	53.6	726	81 A46598	A46598 Sequence 29
15	485.6	53.4	738	81 A46592	A46592 Sequence 23
16	485.6	53.4	738	81 AR063194	AR063194 Sequence
17	483.8	53.2	726	81 A46594	A46594 Sequence 25
18	483.8	53.2	726	81 AR063195	AR063195 Sequence
19	483	53.1	3970	12 ASY14585	Y14585 Artificial
20	479.6	52.8	732	81 A46588	A46588 Sequence 19
21	479.6	52.8	732	81 A46600	A46600 Sequence 31



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 31, 2001, 10:10:13 ; Search time 559.48 Seconds  
(without alignments)  
11385.226 Million cell updates/sec

Title: US-09-424-705-1

Perfect score: 909

Sequence: 1 gaattcataaagagagaa.....atcacatcactaatctaga 909

Scoring table:

IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 7991742 seqs, 3503743858 residues

To: number of hits satisfying chosen parameters: 15983484

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_est3:\*  
4: gb\_est4:\*  
5: gb\_est5:\*  
6: gb\_est6:\*  
7: gb\_est7:\*  
8: gb\_est8:\*  
9: gb\_est9:\*  
10: gb\_est10:\*  
11: gb\_est11:\*  
12: gb\_est12:\*  
13: gb\_est13:\*  
14: gb\_est14:\*  
15: gb\_est15:\*  
16: gb\_est16:\*  
17: gb\_est17:\*  
18: gb\_est18:\*  
19: gb\_est19:\*  
20: gb\_est20:\*  
21: gb\_est21:\*  
22: gb\_est22:\*  
23: gb\_est23:\*  
24: gb\_est24:\*  
25: gb\_est25:\*  
26: gb\_est26:\*  
27: gb\_est27:\*  
28: gb\_est28:\*  
29: gb\_est29:\*  
30: gb\_est30:\*  
31: gb\_est31:\*  
32: gb\_est32:\*  
33: gb\_est33:\*  
34: gb\_est34:\*  
35: gb\_est35:\*  
36: gb\_est36:\*  
37: gb\_est37:\*  
38: gb\_est38:\*  
39: gb\_est39:\*  
40: gb\_est40:\*  
41: em\_estba:\*  
42: em\_estfun:\*  
43: em\_esthum1:\*

44: em\_esthum2:\*  
45: em\_esthum3:\*  
46: em\_esthum4:\*  
47: em\_esthum5:\*  
48: em\_esthum6:\*  
49: em\_esthum7:\*  
50: em\_esthum8:\*  
51: em\_esthum9:\*  
52: em\_esthum10:\*  
53: em\_esthum11:\*  
54: em\_esthum12:\*  
55: em\_esthum13:\*  
56: em\_esthum14:\*  
57: em\_esthum15:\*  
58: em\_esthum16:\*  
59: em\_esthum17:\*  
60: em\_esthum18:\*  
61: em\_esthum19:\*  
62: em\_esthum20:\*  
63: em\_esthum21:\*  
64: em\_esthum22:\*  
65: em\_esthum23:\*  
66: em\_esthum24:\*  
67: em\_esthum25:\*  
68: em\_esthum26:\*  
69: em\_esthum27:\*  
70: em\_esthum28:\*  
71: em\_esthum29:\*  
72: em\_esthum30:\*  
73: em\_esthum31:\*  
74: em\_esthum32:\*  
75: em\_esthum33:\*  
76: em\_esthum34:\*  
77: em\_esthum35:\*  
78: em\_esthum36:\*  
79: em\_esthum37:\*  
80: em\_esthum38:\*  
81: em\_esthum39:\*  
82: em\_esthum40:\*  
83: em\_esthum41:\*  
84: em\_esthum42:\*  
85: em\_esthum43:\*  
86: em\_esthum44:\*  
87: em\_esthum45:\*  
88: em\_esthum46:\*  
89: em\_esthum47:\*  
90: em\_esthum48:\*  
91: em\_esthum49:\*  
92: em\_esthum50:\*  
93: em\_esthum51:\*  
94: em\_esthum52:\*  
95: em\_esthum53:\*  
96: em\_esthum54:\*  
97: em\_esthum55:\*  
98: em\_esthum56:\*  
99: em\_esthum57:\*  
100: em\_esthum58:\*  
101: em\_esthum59:\*  
102: em\_esthum60:\*  
103: em\_esthum61:\*  
104: em\_esthum62:\*  
105: em\_esthum63:\*  
106: em\_esthum64:\*  
107: em\_esthum65:\*  
108: em\_esthum66:\*  
109: em\_esthum67:\*  
110: em\_esthum68:\*  
111: em\_esthum69:\*  
112: em\_esthum70:\*  
113: em\_esthum71:\*  
114: em\_esthum72:\*  
115: em\_esthum73:\*  
116: em\_esthum74:\*

117: em\_estp16:\*  
 118: em\_estp17:\*  
 119: em\_estp18:\*  
 120: em\_estp19:\*  
 121: em\_estp20:\*  
 122: em\_estp21:\*  
 123: em\_estp22:\*  
 124: em\_estp23:\*  
 125: em\_estp24:\*  
 126: em\_estp25:\*  
 127: em\_estp26:\*  
 128: em\_estp27:\*  
 129: em\_estp28:\*  
 130: em\_estp29:\*  
 131: em\_estp30:\*  
 132: em\_estp31:\*  
 133: em\_estp32:\*  
 134: em\_estp33:\*  
 135: em\_estp34:\*  
 136: em\_estp35:\*  
 137: em\_estp36:\*  
 138: em\_estp37:\*  
 139: em\_estp38:\*  
 140: em\_estp39:\*  
 141: em\_estp40:\*  
 142: em\_estp41:\*  
 143: em\_estp42:\*  
 144: em\_estp43:\*  
 145: em\_estp44:\*  
 146: em\_estp45:\*  
 147: em\_estp46:\*  
 148: em\_estp47:\*  
 149: em\_estp48:\*  
 150: em\_estp49:\*  
 151: em\_estp50:\*  
 152: em\_estp51:\*  
 153: em\_estp52:\*  
 154: em\_estp53:\*  
 155: em\_estp54:\*  
 156: em\_estp55:\*  
 157: em\_estp56:\*  
 158: em\_estp57:\*  
 159: em\_estp58:\*  
 160: em\_estp59:\*  
 161: em\_estp60:\*  
 162: em\_estp61:\*  
 163: em\_estp62:\*  
 164: em\_estp63:\*  
 165: em\_estp64:\*  
 166: em\_estp65:\*  
 167: em\_estp66:\*  
 168: em\_estp67:\*  
 169: em\_estp68:\*  
 170: em\_estp69:\*  
 171: em\_estp70:\*  
 172: em\_estp71:\*  
 173: em\_estp72:\*  
 174: em\_estp73:\*  
 175: em\_estp74:\*  
 176: em\_estp75:\*  
 177: em\_estp76:\*  
 178: em\_estp77:\*  
 179: em\_estp78:\*  
 180: em\_estp79:\*  
 181: em\_estp80:\*  
 182: em\_estp81:\*  
 183: em\_estp82:\*  
 184: em\_estp83:\*  
 185: em\_estp84:\*  
 186: em\_estp85:\*  
 187: em\_estp86:\*  
 188: em\_estp87:\*  
 189: em\_estp88:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	DB ID	Description
1	292.6	32.2	472 106	BE289692 601088922
2	287.8	31.7	406 139	BF016722 uY3412.Y
3	283	31.1	396 10	AA691311 vS14f01.r
4	259.6	28.6	413 110	BE624609 uU24c05.Y
5	258.8	28.5	739 106	BE284158 601099428
6	257.8	28.4	644 106	BE281961 601099518
7	254	27.9	358 136	BE850886 uW89h05.Y
8	253	27.8	464 107	BE368025 601211914
9	251.8	27.7	620 107	BE368918 601211562
10	250.4	27.5	401 139	BF015569 uY23c09.Y
11	249.2	27.4	507 139	BF015548 uY23a08.Y
12	247.6	27.2	432 159	AC080097 T135654b
13	247.6	27.2	1057 106	BE306420 601103347
14	243.6	26.8	408 139	BF016419 uY41a08.Y
15	236.8	26.1	473 106	BE307170 601098164
16	233.6	25.7	596 106	BE310080 601091549
17	232.4	25.6	554 174	AZ505978 1M0346J22
18	232	25.5	567 106	BE287568 601097304
19	231	25.4	911 106	BE286958 601092470
20	227	25.0	512 139	BF023434 uX08B04.Y
21	225.6	24.8	379 96	AW908776 uF57d02.Y
22	224	24.6	439 104	BE136816 uG56b01.Y
23	222.2	24.4	634 107	BE371032 601219645
24	220.4	24.2	601 172	AZ447391 1M0244H01
25	215.8	23.7	344 9	AA592800 vO25g11.r
26	214.6	23.6	443 139	BF015986 uY25612.Y
27	209.2	23.0	448 90	AW402665 uI-HF-BKO
28	207.2	22.8	380 23	A1641928 vQ50c10.Y
29	206.4	22.7	549 136	BF022578 uY51a07.Y
30	204.2	22.5	427 136	BE848915 uV90f01.Y
31	200.6	22.1	310 17	A1180569 uC70f09.r
32	200	22.0	398 87	AW228956 uG60c09.Y
33	198	21.8	688 172	AZ399191 1M0164K24
34	197.6	21.7	293 30	AV052316 AV052316
35	196.6	21.6	477 90	AW403686 uI-HF-BKO
36	195.4	21.5	517 90	AW408270 uI-HF-BKO
37	192.8	21.2	485 90	AW403940 uI-HF-BKO
38	189.6	20.9	542 90	AW405977 uI-HF-BKO
39	188.6	20.7	510 90	AW403806 uI-HF-BKO
40	188.4	20.7	488 90	AW403591 uI-HF-BKO
41	187.2	20.6	457 90	AW405627 uI-HF-BLO
42	185.2	20.4	294 14	A1007196 uA73g04.r
43	183.8	20.2	419 90	AW402189 uI-HF-BKO
44	183.8	20.2	639 107	BE371136 601218628
45	183.6	20.2	460 90	AW406939 uI-HF-BLO

## ALIGNMENTS

RESULT 1  
 BE289692 LOCUS BE289692 472 bp mRNA  
 DEFINITION 601088922F1 NCI\_CGAP\_Mam5 Mus musculus cdna clone IMAGE:3483797 5',  
 mRNA sequence.  
 ACCESSION BE289692  
 VERSION BE289692.1 GI:9170234  
 KEYWORDS EST.  
 SOURCE house mouse.





```

Db      61  ttgctgcgtcgcagcctcagccagccatgagcagctgcagcagctcagcagctcggcct 120
Qy      121  gaactggcaaaactcgggctcagtgagaatgtctcgcagggctctcgtctacacctt 180
Db      121  gaaactggcaaaactcgggctcagtgagaatgtctcgcagggctctcgtctacacctt 180
Qy      181  actagttcacagatcagcttggttaaaacagagggcttgacagggcttggaattgga 240
Db      181  actagttcacagatcagcttggttaaaacagagggcttgacagggcttggaattgga 240
Qy      241  tacattacatccagtcggtgtatatactaatatacagaagttcaagaagagccaca 300
Db      241  tacattacatccagtcggtgtatatactaatatacagaagttcaagaagagccaca 300
Qy      301  ttgactaagaagaatctctcagcagacagctacatgcagcagcagcctgacatcag 360
Db      301  ttgactaagaagaatctctcagcagacagctacatgcagcagcagcctgacatcag 360
Qy      361  gactcgcagctatctactgtgcagaatataatgataatgataatgataatgataat 420
Db      361  gactcgcagctatctactgtgcagaatataatgataatgataatgataatgataat 420
Qy      421  ggcaagggcaccactctacagctctcagcagcagcagcagcagcagcagcagcag 480
Db      421  ggcaagggcaccactctacagctctcagcagcagcagcagcagcagcagcagcag 480
Qy      481  gaatttcagaagcagcagctagatagtgatctgctacagctctcagcagcagcag 540
Db      473  -----ggcggtgatactgtgtcagcagcagcagcagcagcagcagcagcag 516
Qy      541  tctcagggaggaagtcacatcagcagcagcagcagcagcagcagcagcagcagcag 588
Db      517  tctcagggaggaagtcacatcagcagcagcagcagcagcagcagcagcagcagcag 576
Qy      589  ---agttacatgaaactgtgtaccagcagaagtcagcagcagcagcagcagcagcag 645
Db      577  gatagttatgtgaactgtgtaccagcagaagtcagcagcagcagcagcagcagcag 636
Qy      646  gacacatccaaactcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt 705
Db      637  gatcattccaaactcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt 696
Qy      706  tctactctccacaaatcagcagcagcagcagcagcagcagcagcagcagcagcagcag 765
Db      697  gactcaccctcaacatcagcagcagcagcagcagcagcagcagcagcagcagcagcag 756
Qy      766  cagtggagtagtaaccatcagcagcagcagcagcagcagcagcagcagcagcagcagcag 825
Db      757  caaagtactcagagtagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 816
Qy      826  gatctgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 885
Db      817  gatctgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 876
Qy      886  caccatcaccatcactaa 903
Db      877  caccatcaccatcactaa 894

```

```

OS      Synthetic.
XX      DE19819846-A1.
PN      11-NOV-1999.
PD      05-MAY-1998; 98DE-1019846.
PE      05-MAY-1998; 98DE-1019846.
PR      05-MAY-1998; 98DE-1019846.
PX      (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PA      Little M, Kipriyanov S;
PI      WPI: 2000-024472/03.
DR      WPI: 2000-024472/03.
XX      Multivalent Fv-antibody constructs with at least four variable domains
PT      connected by 1, 2 and 3 peptide linkers
PS      Example 1; Fig 6; 14pp; German.
XX      This invention describes a novel multivalent Fv-antibody construct with
CC      at least four variable domains that are connected to one another by 1,
CC      2 and 3 peptide linkers. The construct has antiviral, antibacterial
CC      and cytostatic activity. The multivalent Fv-antibody constructs are
CC      useful for the diagnosis and/or therapy of disease, especially viral,
CC      bacterial or tumor diseases. The multivalent Fv-antibody constructs have
CC      increased stability when in the form of a single chain dimer. This
CC      sequence encodes a tetravalent Fv antibody construct composed of the
CC      antibody 9E10 epitope in expression plasmid pDISC319-SL
XX      Sequence 1653 BP; 432 A; 429 C; 424 G; 368 T; 0 other;
SQ

```

Query Match 68.8%; Score 625.4; DB 21; Length 1653;  
Best Local Similarity 85.9%; Pred. No. 1.5e-164;  
Matches 733; Conservative 0; Mismatches 81; Indels 39; Gaps 2;

```

Qy      72  ggcaactcagcggcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 131
Db      825  ggccgctgtgtggccagggctcgcaagtcgcaagtcgcaagtcgcaagtcgcaagtcgcaag 884
Qy      132  acctgggctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 191
Db      885  gactgggctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 944
Qy      192  gatcactcgtgtaaacagagggctcgacagggcttggaatgattgatacatatcc 251
Db      945  gatgaactcgtgtgaaacagagggctcgacagggcttggaatgattgatacatatgccc 1004
Qy      252  tagccgtgtgtatactaatatacagaagttcaagaagcagcagcagcagcagcagcagcag 311
Db      1005  tggagatgtgtatactaatatacagaagttcaagaagcagcagcagcagcagcagcagcag 1064
Qy      312  caaactccacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 371
Db      1065  cgaatccctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1124
Qy      372  ctattactcgtcagatatta-----tgatgatactatacagccttgacta 416
Db      1125  ctattctgttcagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1184
Qy      417  ctggggcagaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 476
Db      1185  ctgggggtcagaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1240
Qy      477  aggtgaatttcagaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 536
Db      1241  -----ggcggtgatactcgtgtcactcagcagcagcagcagcagcagcagcagcagcag 1280
Qy      537  tgcatctcaggggagagagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 596
Db      1281  tgcatctcaggggagagagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1340

```

```

RESULT 3
ID      243432
XX      243432 standard; DNA; 1653 BP.
AC      243432;
XX      18-FEB-2000 (first entry)
DT      Fv-antibody construct containing antibody 9E10 epitope DNA.
XX      Multivalent; Fv-antibody; antiviral; antibacterial; cytostatic;
KM      diagnosis; therapy; disease; ss.
XX

```







KW antibody; autoimmune disease; cancer cell; ss.  
 XX  
 OS Chimeric - Pseudomonas.  
 OS Chimeric - Mammalia.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..1797  
 FT 1.352  
 FT misc\_feature  
 FT /tag= b  
 FT /note= "encodes mature variable domain of the heavy chain"  
 FT misc\_feature 353..396  
 FT /tag= c  
 FT /note= "linker"  
 FT misc\_feature 397..714  
 FT /tag= d  
 FT /note= "encodes mature variable domain of the light chain"  
 FT misc\_feature 715..1797  
 FT /tag= e  
 FT /note= "encodes amino acids 253-613 of PE40"  
 XX  
 XX US5696237-A.  
 PD 09-DEC-1997.  
 XX  
 XX 05-JUN-1995; 95US-0463163.  
 XX  
 PR 21-APR-1989; 89US-0341361.  
 PR 24-SEP-1986; 86US-0911227.  
 PR 08-APR-1992; 92US-0865722.  
 XX  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 PI Chaudhary VK, Fitzgerald D, Pastan IH, Queen CL;  
 PI Waldmann TA;  
 XX  
 DR WPI: 1998-041352/04.  
 DR P-PSDB: W37132.  
 XX  
 PT Antibody toxin fusion proteins - useful as immuno:toxin for  
 XX treating, e.g. lymphocytes associated with auto:immune disease  
 PS Disclosure; Columns 13-18; 20pp; English.  
 XX  
 CC The present sequence encodes a protein that is an example of a novel  
 CC antibody-pseudomonas exotoxin (PE) fragment recombinant fusion protein.  
 CC It is designated anti-Tac(Fv)-PE40. The present fusion gene encodes  
 CC various domains of the heavy chain (the first 116 amino acids), a 15  
 CC amino acid linker, VL-variable domain of the light chain (first 106 amino  
 CC acids), and amino acids 253-613 of PE. This PE fragment possesses  
 CC translocating and ADP ribosylating activity. The fusion gene is cloned  
 CC under the control of a T7 promoter linked to Shine-Delgarno region and  
 CC initiation codon. The fusion protein selectively inhibits protein  
 CC synthesis in cells expressing the interleukin-2 receptor. The  
 CC antibody-PE40 fusion protein is used as an immunotoxin for killing  
 CC cells bearing a receptor or antigen to which the antibody binds.  
 CC e.g. lymphocytes associated with autoimmune diseases or cancer cells.  
 XX  
 SQ Sequence 1797 BP; 336 A; 598 C; 571 G; 292 T; 0 other;

Query Match 58.0%; Score 527.4; DB 19; Length 1797;  
 Best Local Similarity 84.8%; Pred. NO. 2.7e-137;  
 Matches 620; Conservative 0; Mismatches 96; Indels 15; Gaps 2;

QY 93 gcaagtcagcgtcagcagtcgtggcgtgaactgcaagactggggcctcagtgaaagt 152  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 3 gcaggtcagcgtcagcagtcgtggcgtgaactgcaagactggggcctcagtgaaagt 62  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 QY 153 gtccctgcaagcgtctctgtgctaaccttactagttacaagatgcatggtgtaaacagag 212  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 63 gtccctgcaagcgtctctgtgctaaccttactagttacaagatgcatggtgtaaacagag 122  
 QY 213 gctcgtgcaagcgtctgtgatatgattgtgatataatctctgacgtgttatataatta 272  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 123 gctcgtgcaagcgtctgtgatatgattgtgatataatctctgacgtgttatataatta 182  
 QY 273 caatcagaagttcaagcaagcaagccacattgactaacacaacatcctccacacagacct 332  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 183 caatcagaagttcaagcaagcaagccacattgactaacacaacatcctccacacagacct 242  
 QY 333 catgcaactgagcagcctgacatctgagagactctgcagctctattactgtgcaagata 392  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 243 catgcaactgagcagcctgacatctgagagactctgcagctctattactgtgcaagag 302  
 QY 393 tgatgatcatctaacagccttgactctctggggcgaagcaccctctacagctctcgaac 452  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 303 ggggg-----cttgactactctgggccaaggaacacctccacagctctccgcg 352  
 QY 453 caaacaacacccaagcttgaagaagtgtaatttcagaagcacgcgtgatatcgtgct 512  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 353 -----gaggcgtgtgtcgtcgtggcgtggtgcgtcgtggcggtcgtcctcaatgttct 407  
 QY 513 cactcagctcccaagcaatcatgtctgcatctcccaagggaagaagtcacacatgacctgcag 572  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 408 caccacgtctcccaagcaatcatgtctgcatctcccaagggaagaagtcacacatgacctgcag 467  
 QY 573 tgcgaagctcaagtgtaagtctatgactgtgtaccagagcaagtcacactcccca 632  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 468 tgcgaagctcaagtgtaagtctatgactgtgtaccagagcaagtcacactcccca 527  
 QY 633 aagatgtgattatgacaacatcacaactgtctctgagctccctcactcacaaggcgag 692  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 528 actctgtgattataccaatccaactcgtctctgagctccctcactcacaaggcgag 587  
 QY 693 tgggtctgggaacctctactctctcacaatcagcgcatggaagctgaagatgtctgcac 752  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 588 tggatctgggaacctctactctctcacaatcagcgcatggaagctgaagatgtctgcac 647  
 QY 753 ttattactgcagcagtgagtagtaaccatcacgtctgcgtcgaggaacaagttgga 812  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 648 ttattactgcagcagtgagtagtaaccatcacgtctgcgtcgaggaacaagttgga 707  
 QY 813 aataaccggg 823  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 708 gctcaaggcg 718

RESULT 7  
 A10398  
 ID A10398 standard; DNA; 1797 BP.  
 XX  
 AC A10398;  
 XX  
 DT 03-JUL-2000 (first entry)  
 XX  
 DE Recombinant DNA encoding anti-Tac(Fv)-PE40 fusion protein.  
 XX  
 XX Antibody-toxin fusion protein; single chain antibody; immunotoxin;  
 KW Pseudomonas exotoxin; anti-Tac(Fv)-PE40; targeted delivery;  
 KW Interleukin-2 receptor; IL-2; helper T-lymphocyte; autoimmune disease;  
 KW leukaemia; ds.  
 XX  
 OS Chimeric - Pseudomonas sp.  
 OS Chimeric - Mus sp.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..1797  
 FT /tag= a  
 FT /product= "Anti-Tac(Fv)-PE40 immunotoxin  
 FT /note= "No stop codon given in the specification"  
 FT /transl\_except= (pos:1174..1176, aa:Asp)  
 XX  
 PN US6051405-A.

XX 18-APR-2000.  
 PD 08-APR-1992; 92US-0865722.  
 XX 21-APR-1989; 89US-0341361.  
 PF 24-SEP-1986; 86US-0911227.  
 PR (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 PA (PROT-) PROTEIN DESIGN LABS INC.  
 XX  
 XX Fitzgerald D, Chaudhary VK, Pastan IH, Queen CL, Waldmann TA;  
 DR WPI: 2000-363771/31.  
 P-PSDB: Y87477.  
 XX  
 PT Construct encoding recombinant scFV-toxin fusion protein to selectively  
 PT kill cells bearing antigens or receptors comprises DNA segment -  
 XX  
 PS Claim 9; Columns 9-12; 14pp; English.  
 XX  
 CC This sequence represents DNA encoding a recombinant single chain  
 CC antibody fusion protein anti-Tac(Fv)-PE40, which comprises the heavy and  
 CC light chain variable regions (VH and VL) of an anti-Tac antibody and  
 CC residues 253-613 of Pseudomonas exotoxin (Pe). The anti-Tac single chain  
 CC antibody component of the immunotoxin binds to the p55 subunit (Tac  
 CC antigen) of the interleukin-2 (IL-2) receptor, which is present in large  
 CC amounts on helper T-lymphocytes. This enables the cytotoxic action of  
 CC PE40 to be targeted to these and other cell types which express the IL-2  
 CC receptor. The recombinant immunotoxin of the invention may be used to  
 CC treat a variety of autoimmune diseases, including graft-versus-host  
 CC disease, organ transplant rejection, type I diabetes, multiple  
 CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus and  
 CC myasthenia gravis. It may also be used in the treatment of leukaemia,  
 CC and may be used in vitro for the elimination of harmful cells from bone  
 CC marrow before transplant. Anti-Tac(Fv)-PE40 is more active on a molar  
 CC basis than anti-Tac antibody chemically conjugated to full-length PE  
 CC (anti-Tac-Pe) or to PE40 (anti-Tac-PE40).  
 CC  
 XX Sequence 1797 BP; 336 A; 599 C; 570 G; 292 T; 0 other:

Query Match 58.0%; Score 527.4; DB 21; Length 1797;  
 Best Local Similarity 84.8%; Pred. No. 2.7e-137;  
 Matches 620; Conservative 0; Mismatches 96; Indels 15; Gaps 2;  
 QY 93 gcaagtgcaagctgcagcagctctgggctggaactgcaagactgggctcagtgaaat 152  
 D 3 gcaagtgcaagctgcagcagctctgggctggaactgcaagactgggctcagtgaaat 62  
 QY 153 gtcctgcaagctctgctctacaccttactagtagcacagatcgactgggttaaacaag 212  
 Db 63 gtcctgcaagctctgctctacaccttactagtagcacagatcgactgggttaaacaag 122  
 QY 213 gtcctgcaagctctgctctacaccttactagtagcacagatcgactgggttaaacaag 272  
 Db 123 gtcctgcaagctctgctctacaccttactagtagcacagatcgactgggttaaacaag 182  
 QY 273 gtcctgcaagctctgctctacaccttactagtagcacagatcgactgggttaaacaag 332  
 Db 183 gtcctgcaagctctgctctacaccttactagtagcacagatcgactgggttaaacaag 242  
 QY 333 catgcaactgcaagctctgcaactgcaactgcaactgcaactgcaactgcaactgcaact 392  
 Db 243 catgcaactgcaagctctgcaactgcaactgcaactgcaactgcaactgcaactgcaact 302  
 QY 353 tgatgataactaagccttgactctggggccaaggaacacactctacagctctcctcagc 452  
 Db 303 gggggg-----ctctgactactggggccaaggaacacactctacagctctcctcagc- 352  
 QY 453 caaacaac 512  
 Db 353 -----gaagcggtgctcgcgctcgctcgctcgctcgctcgctcgctcgctcgctcgct 407

QY 513 cactcagctcccaagaatcatgtctgcacatcccaaggaggaaggtcacatgactgcag 572  
 Db 408 caccagctctccgaatcatgtctgcacatcccaaggaggaaggtcacatgactgcag 467  
 QY 573 tgcacgctcaagtgtaagttaactgtagtcacagcagaagtaggaagcactcccca 632  
 Db 468 tgcacgctcaagtgtaagttaactgtagtcacagcagaagtaggaagcactcccca 527  
 QY 633 aagatgatttaagcacatcccaactgctctgagctccctgacttaaggggcag 692  
 Db 528 actctgatttaac 587  
 QY 693 tgggtctgggaactcttactctcacaatccagcgagctggaagtagtctgcac 752  
 Db 588 tggatctgggaactcttactctcacaatccagcgagctggaagtagtctgcac 647  
 QY 753 ttattactgcagcagtgtagtagtaaccatcagcttgcgtcgggacaagtgg 812  
 Db 648 ttattactgcagcagtgtagtagtaaccatcagcttgcgtcgggacaagtgg 707  
 QY 813 aataaccggg 823  
 Db 708 gctcaaggcg 718  
 RESULT 8  
 ID Q90663 standard; DNA: 810 BP.  
 AC Q90663;  
 XX 26-JAN-1996 (first entry)  
 DT MFE-23 antibody coding sequence.  
 DE MFE-23 antibody coding sequence.  
 XX Antibody; MFE-23; carcinoembryonic antigen; CEA; colorectal tumour;  
 KW therapy; diabody; ds.  
 XX  
 OS Mus musculus.  
 XX  
 FH Key Location/Qualifiers  
 FT misc\_feature 79..438  
 FT misc\_feature /tag= a  
 FT misc\_feature /note= "variable heavy chain"  
 FT misc\_feature /tag= b  
 FT misc\_feature /note= "linker region"  
 FT misc\_feature 484..801  
 FT misc\_feature /tag= c  
 FT misc\_feature /note= "variable light chain"  
 XX  
 PN W09515341-A1.  
 XX  
 PD 08-JUN-1995.  
 XX  
 PF 05-DEC-1994; 94WO-GB02658.  
 XX  
 PR 03-DEC-1993; 93GB-0024807.  
 XX  
 PA (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.  
 XX  
 PI Begent RHD, Chester KA, Hawkins RE;  
 DR WPI: 1995-215234/28.  
 DR P-PSDB: R75719.  
 XX  
 PT Antibody for carcinoembryonic antigen - for treatment and diagnosis  
 PT of colorectal cancer  
 XX  
 PS Claim 3; Page 48-49; 72pp; English.  
 CC This sequence represents the coding sequence for the MFE-23 antibody.

The encoded protein is an antibody against carcinoembryonic antigen (CEA). CEA is a marker antigen for cancer imaging and therapy. The MFE-23 antibody sequence was obtained using phage technology. In this process, mice were immunised with CEA. The antibody variable region genes obtained from these mice were then amplified from cDNA and cloned as a single chain Fv (scFv) into bacteriophage vectors, producing a library. The phages that bound to biotinylated CEA were selected and amplified, and this sequence (and the protein it encodes) were selected. The MFE-23 antibody was found to have good specificity and affinity for CEA, meaning that it can be used in targeted anti-tumour therapies. A humanised antibody with the complementarity determining regions of MFE-23 may be made by CDR grafting. The antibody may be used for the treatment by surgery or therapy of a colorectal tumour, or in the diagnosis of a colorectal tumour. MFE-23 may also be used to make diabodies (bivalent or bispecific antibody fragments which bind to two different antigens), and may be linked to an antitumour agent or a detectable label.

Sequence 810 BP; 189 A; 220 C; 222 G; 179 T; 0 other:

Best Match 56.7%; Score 515.2; DB 16; Length 810;  
Best Local Similarity 78.9%; Pred. No. 5.1e-134;  
Matches 642; Conservative 0; Mismatches 103; Indels 9; Gaps 2;

16 gagaaataacatgaataacatctatctgctacagcagcgtggtgctgctgctgca 75  
1 gagcagctcatatgaataacatctatctgctacagcagcgtggtgctgctgca 60  
76 gctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 135  
61 gccacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 120  
136 gggcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 195  
121 gggcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 180  
196 cactgggtaaaacagagcagcagcagcagcagcagcagcagcagcagcagc 255  
181 cactgggtaaaacagagcagcagcagcagcagcagcagcagcagcagcagc 240  
256 cgtggtatataatataatataatataatataatataatataatataatataat 315  
241 aatgggtatataatataatataatataatataatataatataatataatataat 300  
316 tccccaacacagcagcagcagcagcagcagcagcagcagcagcagcagcagc 375  
301 tccccaacacagcagcagcagcagcagcagcagcagcagcagcagcagcagc 360  
376 tactg---tgcaagatatattgatgatcattacagcagcagcagcagcagc 432  
361 tattgtaataggaggagcagcagcagcagcagcagcagcagcagcagcagc 420  
433 actctcaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 492  
421 acggctacacgctctctcag-----gtggaggcggttcaggcgagggtgctcggcgt 474  
493 gcaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 552  
475 gggcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 534  
553 aaggtcacacatgaatctgagcagcagcagcagcagcagcagcagcagcagc 612  
535 aaggtcacacatgaatctgagcagcagcagcagcagcagcagcagcagcagc 594  
613 aagtcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 672  
595 aagtcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 654  
673 cctgctcaactcaaggaggaggggtctgaggacaccttaactctccacaataagcagcagc 732  
655 cctgctcaactcaaggaggaggggtctgaggacaccttaactctccacaataagcagcagc 714  
733 gaggctgaagatgctgcaacttattactgcagcagcagcagcagcagcagcagc 792

Db 715 gagcgtgaagatgctgcaacttattactgcagcagcagcagcagcagcagcagcagc 774  
Qy 793 ggtcgtgggagcaagatgtggaataacaggcggc 826  
Db 775 ggtcgtgggagcaagatgtggaataacaggcggc 808

RESULT 9  
ID X00812 standard; DNA; 1797 BP.  
XX X00812;  
AC X00812;  
XX 23-MAR-1999 (first entry)  
DT 23-MAR-1999 (first entry)  
XX Vm-VI-Linker-PE40 DNA segment encoding anti-Tac(Fv)-PE40 fusion protein.  
XX Antibody toxin fusion protein; receptor; immunotoxin; scFv; PE40;  
KW fusion protein; single-chain Fv; Pseudomonas; exotoxin; translocating;  
KW ADP-ribosylating; autoimmune disease; cancer; anti-Tac(Fv)-PE40; ss.  
XX OS Synthetic.  
OS Pseudomonas sp.  
XX Key Location/Qualifiers  
FH 1..1797  
FT CDS  
FT /\*tag- a  
FT /transl\_except- (pos:79..82, aa:Gly)  
FT /transl\_except- (pos:274..276, aa:Ser)  
FT /transl\_except- (pos:295..297, aa:Arg)  
FT /transl\_except- (pos:313..315, aa:Asp)  
FT /transl\_except- (pos:352..354, aa:Gly)  
FT /transl\_except- (pos:370..372, aa:Gly)  
FT /transl\_except- (pos:442..444, aa:Gly)  
FT /transl\_except- (pos:523..525, aa:Pro)  
FT /transl\_except- (pos:529..531, aa:Leu)  
FT /transl\_except- (pos:589..591, aa:Gly)  
FT /transl\_except- (pos:604..606, aa:Tyr)  
FT /transl\_except- (pos:844..846, aa:Ala)  
FT /transl\_except- (pos:892..894, aa:Ile)  
FT /transl\_except- (pos:919..921, aa:Ser)  
FT /transl\_except- (pos:922..924, aa:Ser)  
FT /transl\_except- (pos:979..981, aa:Thr)  
FT /transl\_except- (pos:1042..1044, aa:Ala)  
FT /transl\_except- (pos:1129..1131, aa:Glu)  
FT /transl\_except- (pos:1180..1182, aa:Ser)  
FT /transl\_except- (pos:1201..1203, aa:Glu)  
FT /transl\_except- (pos:1306..1308, aa:Ile)  
FT /transl\_except- (pos:1318..1320, aa:Gly)  
FT /transl\_except- (pos:1489..1491, aa:Phe)  
FT /transl\_except- (pos:1525..1527, aa:Ala)  
FT /transl\_except- (pos:1633..1635, aa:Ala)  
FT /transl\_except- (pos:1642..1644, aa:Glu)  
FT /transl\_except- (pos:1684..1686, aa:Arg)  
FT /transl\_except- (pos:1684..1686, aa:Arg)  
FT /product= "anti-Tac(Fv)-PE40 fusion protein"  
FT /note= "the stop codon is not indicated"

US863745-A.  
26-JAN-1999.  
05-JUN-1995; 95US-0461825.  
21-APR-1989; 89US-0341361.  
24-SEP-1986; 86US-0911227.  
08-APR-1992; 92US-0865772.  
05-JUN-1995; 95US-0461825.  
(US8 ) US DEPT HEALTH & HUMAN SERVICES.  
Chaundhary VK, Fitzgerald DJ, Pastan IH, Queen CL,  
Waldmann TA;

XX	WPI: 1999-131300/11.
DR	P-PSDB: W95462.
XX	
PT	Killing cells with immunotoxin - comprising recombinant fusion
PT	protein of antibody Fv fragment and truncated Pseudomonas exotoxin
PS	
XX	Disclosure: Columns 9-12; 14pp; English.
XX	
CC	The invention relates to recombinant antibody toxin fusion proteins which
CC	selectively kill cells bearing appropriate antigens or receptors. Killing
CC	cells with immunotoxin comprises contacting cells targeted to be killed
CC	with an antibody-PE40 recombinant fusion protein, where the antibody is a
CC	single-chain Fv fragment (scFv) and the PE40 is a Pseudomonas exotoxin
CC	(PE) fragment that lacks amino acids 1-252 and which has at least the
CC	translocating and ADP-ribosylating activity of PE, where the cells
CC	targeted to be killed have receptors or antigens to which the antibody
CC	binds and the fusion protein has lower toxicity to cells that lack such
CC	receptors or antigens. The method is useful for treating autoimmune
CC	diseases or cancer. The present sequence represents a Vm-VI-linker-PE40
CC	DNA segment encoding an anti-Tac(Fv)-PE40 fusion protein.
XQ	
Sequence	1797 BP; 337 A; 595 C; 571 G; 294 T; 0 other;

Query Match	56.48;	Score 513;	DB 20;	Length 1797;
Best Local Similarity	83.68;	Pred. No. 2.8e-133;		
Matches 611; Conservative	0;	Mismatches 105;	Indels 15;	Gaps 2

QY	93	gctctgtagagcttgcaagagctctgggctctggaactcgtgcaagccctggggccctcagctgaaagat	152
Db	3	gcaagctccaaagctcagacagctctcgaggctcggaactcgtgcaaaaacctggggccctccaaatgaaagat	62
QY	153	gtctctgcaagagctctctgtgctacacaccttactaggttaacacagtcaactcgtgggttaaaacagag	212
Db	63	gtctctgcaagagctctctctgtacacaccttactaggttaacacagtcaactcgtgggttaaaacagag	122
QY	213	gctctggaacaggtctctggaatgagatggtatatactaatctcctagccgctggttatacctaatta	272
Db	123	gctctggaacaggtctctggaatgagatggtatatactaatctcctagccactggttatacctaatta	182
QY	273	caatccagaagttccaaggaacaaagccacatctggaactcagaagaacaaacctccacagcaagctta	332
Db	183	caatccagaagttccaaggaacaaagccacatctggaactcagaagaacaaacctccacagcaagctta	242
QY	333	catgccaactcgaacagcctctgaaatctcgaagactctgcagctctatctactctgtgcaagaataata	392
Db	243	catgccaactcgaacagcctctgaaatctcgaagactctgcagctctatctactctgtgcaagaagggg	302
O	393	tgtatgatactaatcagcctctgtaactctctggggccaaagcgacacacctctcaagatctccctcagc	452
Db	303	ggggg-----tcttccactctctggggccaaagcgacacacctctcaagatctccctcagc-	352
QY	453	caaaacaacacacacagcctctggaagaggttgtaatttccagaagccagcgtagatctcgctc	512
Db	353	-----ccaggcggtgctccggcgctcgtgcgctcgggtggtgcggcgcgctcctcaaatgttctc	407
QY	513	cactcagctctccagcaatcatctgctcagctccagctccaggggagagaaggtcaccaatgacctgcag	572
Db	408	caccagctctccagcaatcatctgctcagctccagcggagagaaggtcaccaatgacctgcag	467
QY	573	tgcacagctcgaaggtgtaaggttaacatgaagactgtgacagccaagaagtctagggacccctcccca	632
Db	468	tgcacagctcgaaggtgtaaggttaacatgaagactgtgctccagccaagaagcaggaactctccgcaa	527
QY	633	aagaatgataatatacacaatccacaacacggtctctcgtgagctccctgctcaacttccaggggcag	692
Db	528	agctcgtgattatataccaacatccacaacactcgtctctcgtgggtccctcgtctcgtctcaagtggcag	587
QY	693	tgggtctcgtggaactccttaactctctccacaatcagcggcagatggaagctgtgaagatcgtccac	752
Db	588	tgcatactggaacactcttaagctctctccacaatcagcggcagatggaagctgtgaagatcgtccac	647

Oy	753	t t a t t a c t g c c a g c a g t g n a g t a a c c a t t a c g t t c g g c t c g g g a c a a g t t g g a	812
Dd	648	t t a t t a c t g c c a c t c a a a g a g t a c t t a c c a c t c a c g t t c g t c g g a c c a a g c t g g a	707
Oy	813	a a t a a c c g g g	823
Dd	708	g c t c a a g g c g	718

RESULT 10

ID T86309 standard; DNA; 717 BP.

AC T86309;

DE Single chain anti-disialoganglioside GD2 antibody 5F11-SCFv.

KM Antibody construct, disialoganglioside; GD2, single chain Fv fragment;  
 KM scFv; tumour; neuroblastoma; osteosarcoma; soft tissue sarcoma;  
 KM tissue imaging; target delivery; toxin; streptavidin;  
 KM pro-drug converting enzyme; GD2-targeted lymphocyte; ss.

OS Synthetic.

PN W09734634-A1.

PD 25-SEP-1997.

PF 20-MAR-1997; 97WO-US04427.

PR 20-MAR-1996; 96US-0013703.

PA (SLOK ) SLOAN KETTERING INST CANCER RES.

PI Cheung NV, Guo H, Larson SM, Rivlin K, Sadelain M;

DR WPI; 1997-479996/44.

PT Recombinant single chain anti-disialoganglioside GD2 antibody -  
PT useful to detect tumour cells expressing GD2 and to target  
PT therapeutic agents, e.g. toxins, to such cells

PS Disclosure; Page 11; 31pp; English.

The present sequence encodes a recombinant single chain peptide, 5F11-scFv. The peptide is an antibody construct comprising the variable regions of the heavy and light chains of an antibody against disialoganglioside (GD2) as a single chain Fv fragment (scFv). GD2 occurs in many tumours types including neuroblastoma, osteosarcomas and other soft tissue sarcomas, medulloblastomas, high grade astrocytomas, melanomas and small cell lung cancer. The peptide can be detectably labelled, preferably with 99mTc, for tissue imaging of cells expressing GD2. It can also be used to target delivery of a therapeutic or pre-therapeutic agent, such as a toxin, streptavidin or a pro-drug converting enzyme, to cells expressing GD2. The peptide may further comprise CD8 to facilitate the formation of GD2-targeted lymphocytes. T cells containing the peptide can also be used to target GD2-producing tumour cells.

Sequence 717 BP; 180 A; 181 C; 195 G; 159 T; 2 other;

Query Match	54.48;	Score 494.2;	DB 18;	Length 717;
Best Local Similarly	81.98;	Pred. No. 3.4e-128;		
Matches 597; Conservative	0;	Mismatches 120;	Indels 12;	Gaps 2

Oy	94	caggtgcagctcagcagctcgtggtcgaaactggaagactggggcctacgtgaatg	153
Db	1	cagtgtaaacctcagcagctcaggaactcgtgnaactcgtgggttcagtgaaata	60
Oy	154	tctctgcaaggtcttggcttaacaccttaactagtgatcacagatgcaactcgtgtaaacagag	213



Dd	595	tctcccaactctggtttatagacataccaacctgcgttcctgtagtccctgcgcgttc	654
Oy	685	aggggacagtgggtctcggagaccctctactctctccaatacagcgagcatgsggtcgaagat	744
Dd	655	attgggcagtgagatcttggagacccttctactctctacaatacagcggaagtggagctgaagat	714
Oy	745	gttcgcacttatctacgcagcgagtgagtagaacccatcacgttcgcgtcgggaca	804
Dd	715	gttcgcacttatctactgcagcaagaagtaacttacccgcctcacgttcggtgcggacc	774
Oy	805	aagttggaataaacccgg	823
Dd	775	aagtcgagatcaacggy	793
RESULT 12			
T86311	ID	T86311 standard; DNA; 1175 BP.	
XX	AC	T86311;	
XX	GC		
XX	TT		
XX	CC		
XX	GG		
XX	AA		
XX	CT		
XX	GA		
XX	TC		
XX	CA		
XX	GT		
XX	TA		
XX	AT		
XX	CG		
XX	AG		
XX	CT		
XX	GA		
XX	TC		
XX	CA		
XX	GT		
XX	TA		
XX	AT		
XX	CG		
XX	AG		
XX	CT		
XX	GA		
XX	TC		
XX	CA		
XX	GT		
XX	TA		
XX	AT		
XX	CG		
XX	AG		
XX	CT		
XX	GA		
XX	TC		
XX	CA		
XX	GT		
XX	TA		
XX	AT		
XX	CG		
XX	AG		
XX	CT		
XX	GA		
XX	TC		
XX	CA		
XX	GT		
XX	TA		
XX	AT		
XX	CG		
XX	AG		
XX	CT		
XX	GA		
XX	TC		
XX	CA		
XX	GT		
XX	TA		
XX	AT		
XX	CG		
XX	AG		
XX	CT		
XX	GA		
XX	TC		
XX	CA		
XX	GT		
XX	TA		
XX	AT		
XX	CG		
XX	AG		
XX	CT		
XX	GA		
XX	TC		
XX	CA		
XX	GT		
XX	TA		
XX	AT		
XX	CG		
XX	AG		
XX	CT		
XX	GA		
XX	TC		
XX	CA		
XX	GT		
XX	TA		
XX	AT		
XX	CG		
XX	AG		
XX	CT		
XX	GA		
XX	TC		
XX	CA		
XX	GT		
XX	TA		
XX	AT		
XX	CG		
XX	AG		
XX	CT		
XX	GA		
XX	TC		
XX	CA		
XX	GT		
XX	TA		
XX	AT		
XX	CG		
XX	AG		
XX	CT		
XX	GA		
XX	TC		
XX	CA		
XX	GT		
XX	TA		
XX	AT		
XX	CG		
XX	AG		
XX	CT		
XX	GA		
XX	TC		
XX	CA		
XX	GT		
XX	TA		
XX	AT		
XX	CG		
XX	AG		
XX	CT		
XX	GA		
XX	TC		
XX	CA		
XX	GT		
XX	TA		
XX	AT		
XX	CG		
XX	AG		
XX	CT		
XX	GA		
XX	TC		
XX	CA		
XX	GT		
XX	TA		
XX	AT		
XX	CG		
XX	AG		
XX	CT		
XX	GA		
XX	TC		
XX	CA		

CC pre-therapeutic agent, such as a toxin, streptavidin (e.g. present  
CC sequence) or a pro-drug converting enzyme, to cells expressing GD2. The  
CC peptide may further comprise C8 to facilitate the formation of  
CC GD2-targeted lymphocytes. T cells containing the peptide can also be used  
CC to target GD2-producing tumour cells.

SQ Sequence 1175 BP; 276 A; 346 C; 330 G; 221 T; 2 other;

Query Match	53.7%;	Score 488.4;	DB 18;	Length 1175;
Best Local Similarity	80.7%;	Pred. No. 1.7e-126;		
Matches 610;	Conservative 0;	Mismatches 133;	Indels 13;	Gaps 3

QY	94	cagggtgcagcgtgcagcgaattctctggggtctgaacttgcgaagaacccctggggccttcagtgaaagt	150
Dp	1	cagggtgaaactgcagcgaattccagcgtgaacctggtgmaagcctctgggtcttcagtgaaagt	60
QY	154	tctctgcagaggtcttcgcgtctaacaccttlaactgtaatacgaatgcgaactggtgttaaacaagagg	210
Dp	61	tctctgcagaggtctctgsmacnaaattcaacttgatataccacatgcgaactggtgtgaagcaggc	120
QY	214	ccctgcagcaggtcttcggaatctggaatctggaatacttaactcctagccggtgttataactaat	270
Dp	121	catggaagaagacctgagtggaattggaagtataacttaacttaaccataatggtgtgtactaactac	180
QY	274	aatcaagaaggttccaaggagaaagggccaacttgatctgaatacagaacaaatctctccagacagccac	330
Dp	181	aagcgaagaaggttccaaggagaaagggccaacttgatctgaatacagaacaaatctctccagacagccac	240
QY	334	atgcgaactgcagcagcctctacactctggaagacactgcgaactctlaactgtgcagaagatatat	390
Dp	241	atggagactccgcagcctgcgaactctgcgaagattctgcgaactctlaactgtgcagaagatat	300
QY	394	gattatcatctacagccttgactacttggggccaagggcaccaactctcaagctctcctcaagcc	450
Dp	301	acggtctccggtctctgactactgtgtctccaagggaccacggtcaacggtctcctcag	350
QY	454	aaaacaacacccaagcgttgaagaagggtgaatttttccaagaagcagcgtgatataatgtgtc	510
Dp	353	-----gtggaagcgggttcagcgcggaaggtgtgctctgcgcgtgtgcggaatcggatctgaagctc	400
QY	514	actcaagttctccaagaatcatgtctgcgaactctccagggggaagaagttcacacatgactgcga	570
Dp	409	actcaagttctccaagaatcatgtctgcgaactctccagggggaagaagttcacacatgactgcga	460
QY	574	gccagcctcaagtgtgaagttaacatgaaactcgtgtaccaaagcagaagttcaagcgaactccccca	630
Dp	469	ggcagcctcaagtgtgaagttaacatgaaactcgtgtaccaaagcagaagcgtgtcaactccccca	520
QY	634	agatggatcttctgacacatcccaaaactggtctcttggaagctccctgtcacttgaaggggcgt	690
Dp	529	agatggatcttctgacacatcccaaaactggtctcttggaagctccctgtcacttgaaggggcgt	580
QY	694	gggtctgcgaacctctcaactctctcaacaatcgaacggaatgcgaagtgagtgactgcgcact	750
Dp	589	gggtctgcgaacctctctcaactctctcaacaatcgaacggaatgcgaagtgagtgactgcgcact	640
QY	754	tattactgtccagcagctggaagtgaatacccatcgaactgcgtctgcgggacaagaattgaa	810
Dp	648	tattactgtccatcagcgggaagtgaatacccgctcaactgcgtctgcgggacaagaattgaa	700
QY	814	ataaacggggtctgatactgcgaacccaactgcgaatccgaa	849
Dp	708	ataaaaacggggtctgatactgcgaacccaactgcgaatccggtgactgcga	743
RESULT 13			
T040025			
ID T04025 standard; cDNA; 726 BP.			
XX T04025;			
AC			
TT 02-JUL-1996 (first entry)			

[illegible]

D	b	242	tgcacactcagcaggctgacatctcgtggagacctcggtgcttactactgycaccagtcgggaact	301
O	y	395	atgatcatlacag-----ecttgactactrgggccaaggcacacctctaacagtctcc	448
D	b	302	atgatctcagcagcaggttactttgactactggygccaaaggacacaggtacacgtctcc	361
O	y	449	cagccaaaacaaccccagaagcttaagaaagtgtatttcagaagcagcgttagatacg	508
D	b	362	caagtcggtcggtggtctc-----gggcggtggtgtggtgtggtgcggtacatgtg	415
O	y	509	tgtccactcagctccccaagcaatactgtctgcactctccaggggagaagtlaccatgact	568
D	b	416	agctcaaccagctcccatcaatactgtctgtacatctccaggggagaaggtacacatgacct	475
O	y	569	gcagctgcacagctcagtgtaagtatactgaactggttacccagcagaagtcagcacctccc	628
D	b	476	gcagltgacagctcaagtcgtaagttacatgtctctgtaccagcagaagaacagatcccc	535
O	y	629	ccaaaagatgtattatygacacatccaacacgtgcttttgagtccctcgctcacttaagg	688
D	b	536	ccagactctctattatlypacacatccacaacctggcttctgagatccctgtctgcctcagt	595
O	y	689	gcagtgggctctgggacctcttactctctccacaatcagcagcatggaagctgaagatgtg	748
D	b	556	gaagtgggctctgggacctcttactctctccacaatcagcagcatggaagctgaagatgtg	655
O	y	749	ccacttatctgcgcagcagtgtagtaagtaaacatccatcagctgcgtcggggacaagt	808
D	b	656	ccacttatctgcgcagcagtgtagtaagtaaacatccacacagcttcgtgcgtcgggaccaag	715
O	y	809	tggaataaa 818	
D	b	716	tggaataaa 725	
RESULT 14				
T040022	ID	T04022 standard; cDNA: 738 BP.		
XX AC	AC	T04022;		
DT XX	XX	02-JUL-1996 (first entry)		
DE XX	XX	Anti-EGFR single chain antibody (Clone 1 E 3).		
KW KM	KM	Single chain antibody; antibody; epidermal growth factor receptor; EGFR; tumour; cancer; glioma; melanoma; carcinoma; diagnosis; assessment; phage antibody library; ss.		
OS XX	XX	Mus musculus.		
FH FT	FT	Key Location/Qualifiers 1..738 /*tag= a CDS /product= Single-chain Fv, heavy and light chain plus linker.		
FT FT	FT			
PN PD	PD	WO9525167-A1.		
XX PF	PF	21-SEP-1995.		
XX PE	PE	16-MAR-1995; 95WO-EP00978.		
XX PR	PR	02-DEC-1994; 94EP-0118970.		
XX PA	PA	17-MAR-1994; 94EP-0104160.		
XX PI	PI	(MERCK ) MERCK PATENT GMBH.		
XX DR	DR	Adan J, Ansell KH, Bendig MM, Blasco F, Guessow D; Kettlborough AC, Mitjans F, Piulats J, Rosell E; WPI: 1995-336972/43. P-PsDB: R79869.		



XX Anti-EGFR antibodies and single chain Fv antibody fragments -  
 PT obtained from phage-antibody libraries, useful for diagnosis and  
 PT therapy of tumours  
 XX  
 PS Claim 4; Page 64-65; 93pp; English.  
 XX  
 CC Anti-epidermal growth factor receptor (EGFR) single chain antibodies  
 CC and antibodies constructed from anti-EGFR antibody fragments can be  
 CC used for diagnosis of tumours and assessment of tumour growth in  
 CC vitro and in vivo. They may also be used in a pharmaceutical  
 CC composition for the therapy of e.g. melanomas, gliomas and carcinomas.  
 CC The antibodies and fragments are derived from mice but are humanised  
 CC so as to cause minimum reaction against them. They are produced  
 CC using the phage antibody library. (See T04011-T04026 and  
 CC R79858-R79873)  
 XX  
 SQ Sequence 738 BP; 174 A; 195 C; 211 G; 158 T; 0 other;

Query Match 53.4%; Score 485.6; DB 16; Length 738;  
 Best Local Similarity 80.8%; Pred. No. 8, 5e-126;  
 Matches 59; Conservative 0; Mismatches 129; Indels 12; Gaps 2;

QY 95 aggtgcagctgcagcagctctggggtgaactgcgaagacctggggcctcagtgaaagtgt 154  
 |||||  
 Db 2 aggtgcagctgcagcagctctggggtgaactgcgaagacctggggcctcagtgaaagtgt 61  
 QY 155 cctgcagagctctgcgtctacaccttactagtgtacagatgcactgggttaaacagagggc 214  
 |||||  
 Db 62 cctgcagagctctgcgtctacaccttactagtgtacagatgcactgggttaaacagagggc 121  
 QY 215 ctgcagaggtctgcgtatgtatgatacattacccctagcgcgtgtataactaattaca 274  
 |||||  
 Db 122 ctgcagaggtctgcgtatgtatgatacattacccctagcgcgtgtataactaattaca 181  
 QY 275 atcagaagttcaagacaagccacattgactacagacaatctccctcagcagagctaca 334  
 |||||  
 Db 182 atcagaagttcaagacaagccacattgactacagacaatctccctcagcagagctaca 241  
 QY 335 tgcacatgcagagctgcagctctgacatctgcagctcttactatgtgcagagatatatg 394  
 |||||  
 Db 242 tgcacatgcagagctgcagctctgacatctgcagctcttactatgtgcagagatatatg 301  
 QY 395 atgactcattacag-----ccttactactggggcgaagcaccatctcagctcct 448  
 |||||  
 Db 302 atgactcattacag-----ccttactactggggcgaagcaccatctcagctcct 361  
 QY 449 cagcacaacaacacacacagcttgaagaaggtgaatttcagaagcagcgtatagatcg 508  
 |||||  
 Db 362 caggtggcgtgtgtcggcggt 421  
 QY 509 tgcctcactagctctccagcaatcatgtctgcattccagggggaagaagtcacatgact 568  
 |||||  
 Db 422 agctcaccacgtctccacaacatcatgtctgcattccagggggaagaagtcacatgact 481  
 QY 569 gcaatgcagctgcagatgaagttaactgaactggtacccaagaagcagcagcctccc 628  
 |||||  
 Db 482 gcaatgcagctgcagatgaagttaactgaactggtacccaagaagcagcagcctccc 541  
 QY 629 ccaaaagtgtgattatgcacatccaaactggtctctgcagtcctcctcacttcaggg 688  
 |||||  
 Db 542 ccagagcccttgattatgcacatccaaactggtctctgcagtcctcctcacttcaggg 601  
 QY 689 gcagtggtctgcagactcttactcttcacaatcagcgggaatggagctgtaaatgctg 748  
 |||||  
 Db 602 gcagtggtctgcagactcttactcttcacaatcagcgggaatggagctgtaaatgctg 661  
 QY 749 ccaacttactgcagcagatgtagtgaacc-----ttcagcttcggcccgaggga 802  
 |||||  
 Db 662 ccaacttactgcagcagatgtagtgaacc-----ttcagcttcggcccgaggga 721  
 QY 803 caaagtgtgaataaa 818

Db 722 ccaagctggaataaa 737

RESULT 15

ID T04023 standard; cDNA; 726 BP.

AC T04023;

DT 02-JUL-1996 (first entry)

DE Anti-EGFR single chain antibody (Clone 5 F 1).

KW Single chain antibody; antibody; epidermal growth factor receptor;

KW EGFR; tumour; cancer; glioma; melanoma; carcinoma; diagnosis;

XX assessment; phage antibody library; ss.

OS Mus musculus.

XX Key

FT CDS Location/Qualifiers

FT CDS 1..726

FT CDS /tag- a

FT CDS /product- Single-chain Fv, heavy and light chain

FT CDS plus linker.

FT CDS

FT CDS

FT CDS

FT CDS

FT CDS

FT CDS

FT CDS

FT CDS

FT CDS

FT CDS

FT CDS

FT CDS

FT CDS

FT CDS

FT CDS

FT CDS

FT CDS

FT CDS

FT CDS

FT CDS

Query Match 53.2%; Score 483.8; DB 16; Length 726;

Best Local Similarity 81.0%; Pred. No. 2, 7e-125;

Matches 59; Conservative 0; Mismatches 127; Indels 12; Gaps 2;

QY 94 caggtgcagctgcagcagctctggggtgaactgcgaagacctggggcctcagtgaaagtgt 153  
 .|||||  
 Db 1 caggtgcagctgcagcagctctggggtgaactgcgaagacctggggcctcagtgaaagtgt 60  
 QY 154 tctctcagagctctcgtctacaccttactaggtacacagatgcagtgagtgaaacagagg 213  
 |||||  
 Db 61 tctctcagagctctcgtctacaccttactaggtacacagatgcagtgagtgagtgagagagg 120

```
QY 214 cctggacaaggctctgggaatgttgatgataatccttagccgtgttactaatlac 273
    ||||| || ||||| ||| ||||| || ||||| || ||||| ||
Db 121 gctggacaaggcctctgagtggaatcggagatataatccagaacgcgctactaac 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 274 aatcaagaattcaagaagacaaagccacatltgactacagacaatcctccagacagctac 333
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 aatgagaattcaagaagcgaagccacacatgacgtgtagacaatcctccagacagctac 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 334 atgcaactgagcagcctgacatctgaggaactctgcagctatactgtgtgaagatatat 393
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 241 atgcaactgagcagcctgacatctgaggaactctgcagctatactgtgtgaagatatat 300
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 394 gatgacatcacag-----ccttgactctggggccaaggccacactccacagctctc 447
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 301 tatgattacgaagcgaagctacttgaactactgaggccaagggaacaagctcacagctctc 360
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 448 tcaagccaacaacacccaagcttgaagaagtgaattttcagaagcacgcgtatgatalc 507
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 361 tcaagtggtggtgtgtc-----gggcggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 414
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 508 gtgtctactcagctctccagcaatcagtctgtcactcccaagggaagaagtcacacatgac 567
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 415 gagctacaccagctctccacaacatcaltgtctgtcctccagggaagaagtlcaccatgacc 474
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 568 tgcagtgccagctcaagtgaatgttacatgaactgtgtaccagcagaagtacggcacctcc 627
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 475 tgcagtgacagctcaagtgaatgttaacgttaacgttaacgttaacgttaacgttaacgt 534
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 628 cccaaaagatggaattatgacacatccaaaatgtgtcttgaagtcctgtcaactcaagg 687
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 535 cccagactcctgtattatgacacatccaaaatgtgtcttgaagtcctgtcaactcaagg 594
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 688 ggcagtggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 747
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 595 ggcagtggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 654
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 748 ggcactatctactgcagcagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 807
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 655 ggcactatctactgcagcagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 714
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 808 ttggaataaa 818
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 715 ctggaataaa 725
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

Session completed: March 31, 2001, 11:57:13  
Time: 3745 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 31, 2001, 10:51:13 ; Search time 56.59 Seconds

(without alignments)  
2588.703 Million cell updates/sec

Title: US-09-424-705-1

Perfect score: 909

Sequence: 1 gaattcataaagagagaa.....atcacatcactatcataga 909

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 280836 seqs, 80580151 residues

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Issued Patents\_NA:\*

- 1: /cgn2\_6/prodata/2/ina/5A\_COMB.seq:\*
- 2: /cgn2\_6/prodata/2/ina/5B\_COMB.seq:\*
- 3: /cgn2\_6/prodata/2/ina/6\_COMB.seq:\*
- 4: /cgn2\_6/prodata/2/ina/PCTUS\_COMB.seq:\*
- 5: /cgn2\_6/prodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	529	58.2	719	3	US-08-279-772A-7
2	529	58.2	720	3	US-08-502-486-10
3	527.4	58.0	1797	1	US-08-463-163-2
4	515.2	56.7	810	2	US-08-652-507-1
5	485.6	53.4	738	2	US-08-553-497A-23
6	483.8	53.2	726	2	US-08-553-497A-25
7	479.6	52.8	732	2	US-08-553-497A-19
8	471.6	51.9	732	2	US-08-553-497A-21
9	468.4	51.5	726	2	US-08-553-497A-27
10	455.8	50.1	1679	2	US-08-601-052-15
11	397.2	43.7	831	2	US-08-403-853-17
12	393.8	43.3	883	3	US-09-184-658-7
13	379.8	41.8	720	2	US-08-800-198-7
14	379.8	41.8	720	3	US-09-296-595-7
15	369.8	40.7	891	2	US-08-894-922A-9
16	368.8	40.6	1570	2	US-08-116-247-6
17	367.2	40.4	1570	2	US-08-303-569B-6
18	365.8	40.2	711	2	US-08-190-199A-64
19	358.8	39.5	708	2	US-08-956-047-24
20	342.8	37.7	708	2	US-08-190-199A-60
21	340.8	37.5	996	2	US-08-894-922A-4
22	337.4	37.1	943	2	US-08-303-569B-4
23	337.4	37.1	943	2	US-08-116-247-4
24	335.8	36.9	672	2	US-08-190-199A-62
25	334.8	36.8	793	2	US-08-956-047-29
26	327.8	36.1	920	2	US-08-860-174A-3
27	326.4	35.9	756	2	US-08-797-689-17
28	326.4	35.9	858	2	US-08-428-257A-71

29	326.4	35.9	858	2	US-08-491-988-2	Sequence 2, Appl
30	326.4	35.9	1257	2	US-08-491-988-8	Sequence 8, Appl
31	326.4	35.9	1259	2	US-08-491-988-10	Sequence 10, Appl
32	326.4	35.9	1236	2	US-08-491-988-6	Sequence 6, Appl
33	326.4	35.9	1356	2	US-08-491-988-4	Sequence 4, Appl
34	326.4	35.9	1648	2	US-08-491-988-13	Sequence 13, Appl
35	314.6	34.6	797	2	US-08-894-922A-13	Sequence 13, Appl
36	312.8	34.4	669	2	US-08-190-199A-66	Sequence 66, Appl
37	304.8	33.5	924	2	US-08-860-174A-9	Sequence 9, Appl
38	303	33.3	2012	1	US-08-235-838-15	Sequence 15, Appl
39	303	33.3	2012	2	US-08-465-473B-15	Sequence 15, Appl
40	302.2	33.2	748	1	US-08-235-838-10	Sequence 10, Appl
41	302.2	33.2	748	1	US-08-465-473B-10	Sequence 10, Appl
42	300.8	33.1	417	2	US-08-656-586-3	Sequence 3, Appl
43	299.8	33.0	384	2	US-08-656-586-1	Sequence 1, Appl
44	299.4	32.9	354	2	US-08-273-146-58	Sequence 58, Appl
45	298.8	32.9	735	4	PCT-US94-14106-50	Sequence 50, Appl

## ALIGNMENTS

RESULT 1  
US-08-279-772A-7  
Sequence 7, Application US/08279772A  
Patent No. 6080560  
GENERAL INFORMATION:  
APPLICANT: Russell, David R  
TITLE OF INVENTION: Method for Producing Antibodies in Plant  
TITLE OF INVENTION: Cells  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESSES:  
ADDRESS: Quarles and Brady  
STREET: PO Box 2113  
CITY: Madison  
STATE: WI  
COUNTRY: United States of America  
ZIP: 53701-2113  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/279,772A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Seay, Nicholas J.  
REGISTRATION NUMBER: 27,386  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 608-251-5000  
TELEFAX: 608-251-9166  
INFORMATION FOR SEQ. ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 719 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..719  
US-08-279-772A-7

Query Match 58.2% Score 529. DB 3: Length 719;  
Best Local Similarity 85.0% Pred. No. 6.8e-154;  
Matches 621: Conservative 0; Mismatches 95; Indels 15; Gaps 2;  
QY 88 atggcgagtgacgtgcagctgctggtgactgcaagcctggtgctcagtg 147



```

Db      586  GGCATGGATCTGGGACCTCTTACTCTCTCATCATCAAGCCAAATGGAGGCTGGAAGATGCT 643
Oy      748  gccacttattctgccagcagtggaagtagtaaaccaattcacgctcggcgggacaag 807
Db      646  GCCACTTATTACTGCGCATCAAGAAGAGTACTTACCACACTACAGTTCGGTCTGGGACCAAG 705
Oy      808  ttggaataaa 818
Db      706  CTGGAGCTCAA 716

RESULT      3
US-08-463-163-2
; Sequence 2, Application US/08463163
; Patent No. 5696237
; GENERAL INFORMATION:
; APPLICANT: Fitzgerald, David J.
; APPLICANT: Chaudhary, Vijay K.
; APPLICANT: Pastan, Ira H.
; APPLICANT: Waldmann, Thomas A.
; APPLICANT: Queen, Cary L.
; TITLE OF INVENTION: Recombinant Antibody-Toxin Fusion Protein
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Stewart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,163
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 06/227,227
; FILING DATE: 22-JAN-1981
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 06/911,227
; FILING DATE: 24-SEP-1986
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/341,361
; FILING DATE: 21-APR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/865,722
; FILING DATE: 08-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen L.
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 015280-12211
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1797 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1797
; OTHER INFORMATION: /product= "Anti-Tac(Fv)-pE40"
US-08-463-163-2

```

[illegible]

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/652,507  
FILING DATE: 02-Jul-1996  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Arthur R. Crawford  
REGISTRATION NUMBER: 25,327  
REFERENCE/DOCKET NUMBER: 117-211  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-816-4100  
TELEFAX: 703-816-4100  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 810 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-652-507-1

Query Match 56.7% Score 515.2; DB 2; Length 810;  
Best Local Similarity 78.9%; Pred No. 1.3e-149;  
Matches 642; Conservative 0; Mismatches 163; Indels 9; Gaps 2;

16 gagaaatlaacacatgaataactatctgctcagcagcagcgtgctgctgctgca 75  
1 GAGACAGTCATATGAATAATCACTATTGCCACGCGCGCTGATTTATATCTCGCG 60  
76 gctcagcgcgcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 135  
61 GCCCAGCCGCGCCATGCGCCAGTGAACAGTCAAGTCTGGCGCAGAACTTGTGAGCTCA 120  
136 gagagcctcagtgagatgctcctcagcagcgtcctgctgctacaccttactagatgacagat 195  
121 GGCACCTCATGATCAAGTTGCTCTCCACAGCTTCTGCTTCAACTTAAAGACTCTTATATG 180  
196 cactgggtlaaacaagagcgtgagcagggctcgtgaaatgagatgatacctaactcagc 255  
181 CACTGTTGAGGAGGAGGCGCTGAACAGGCGCTGAGTGGATGGATGATGATCTCTGAG 240  
256 cgtggttataactaataacaaagcagcagcagcagcagcagcagcagcagcagc 315  
241 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300  
316 tctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 375  
301 TCCCTCCACACACAGCTTACCTGAGCTGACAGCTGACATCTGAGACACTGCGCTAT 360  
376 tactg---tgcaagatatatgatatcattacagccttgaactcagcagcagcagc 432  
361 TATGTGATGAGGAGGAGCTGCGACTGCGCTGACTTGTGACTGAGGCGCCAGGAGACC 420  
433 actctcagcagcctcctcagcagcagcagcagcagcagcagcagcagcagcagcagc 492  
421 ACGGTCACCGCTCCCTCAG-----CTGAGAGCGGCTTCAAGCGAGGAGCTGCTGCGGAT 474  
493 gcaagcgtgagatagtgctcactcagcagcagcagcagcagcagcagcagcagcagc 552  
475 GCGCGATCAAGAAATGTGCTCACCGCTCCAGCATATGCTCATCTCCAGGAGAG 534  
553 aaggtacacatgacccagcagcagcagcagcagcagcagcagcagcagcagcagcagc 612  
535 AAGGTACACATACCTGACAGTGCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAG 594  
613 aagtcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 672  
595 AAGCGAGGACACTTCTCCAAACTCTGATTTATAGCACATCCAACTGCTGCTTGTGAGTTC 654

673 cctgctcactcaggggcagtggtcctggagccttactctcacaatcagcggcagc 732  
655 CCGTCTCGCTTCACTGAGTGGAGTGGAGCTCTTACTCTCTCAGTACAGCCGAAG 714  
733 gagcctgaagatgctgcacattactcgcacagcagtgagtagtaaccatcagcttc 792  
715 GAGGCTGAAGATGCTCCACTTATTAAGTGAAGAGTGAAGTGAAGTGAAGTGAAGTGAAG 774  
793 ggtcgggagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 826  
775 GGTGCTGGCAGCAAGCTGAGCTGAAGACGGGCGG 808  
RESULT 5  
US-08-553-497A-23  
Sequence 23, Application US/08553497A  
Patent No. 5844093  
GENERAL INFORMATION:  
APPLICANT: KETTLEBOROUGH, C. A.  
APPLICANT: BENDIS, MARY M.  
APPLICANT: ANSELL, KEITH H.  
APPLICANT: GUSSON, DETLEF  
APPLICANT: ADAN, JAUME  
APPLICANT: MITJANS, FRANCESCA  
APPLICANT: ROSELL, ELISABET  
APPLICANT: BLASCO, FRANCESCA  
APPLICANT: PUIGATS, JAUME  
TITLE OF INVENTION: ANTI-BGFR SINGLE-CHAIN FVS AND ANTI-BGFR  
TITLE OF INVENTION: ANTIBODIES  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: MILDEN, WHITE, ZEILAND & BRANIGAN, P. C.  
STREET: 2200 CLARENDON BLVD. SUITE 1400  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: US  
ZIP: 22201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/553,497A  
FILING DATE: 17-NOV-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION NUMBER:  
APPLICATION NUMBER: NO PCT/EP95/00978  
FILING DATE: 16-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 94104160.0  
FILING DATE: 17-MAR-1994  
APPLICATION DATA:  
APPLICATION NUMBER: EP 94118970.6  
FILING DATE: 02-DEC-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: HAMLET-KING, DIANA  
REGISTRATION NUMBER: 33,302  
REFERENCE/DOCKET NUMBER: MERCK 1726  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-243-6333  
TELEFAX: 703-243-6410  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 738 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal

```
ORIGINAL SOURCE:
ORGANISM: mouse
STRAIN: Balb/c
TISSUE TYPE: splenocytes
IMMEDIATE SOURCE:
CLONE: 1 E 3 (single-chain Fv, heavy and light chain
FEATURE: plus linker)
NAME/KEY: CDS
LOCATION: 1..738
US-08-553-497A-23
```

```
Query Match      53.4%; Score 485.6; DB 2; Length 738;
Best Local Similarity 80.8%; Pred. No. 1.7e-140;
Matches 595; Conservative 0; Mismatches 129; Indels 12; Gaps 2;
```

```
QY 95 aggtcagctgcagcagctctgggctgaactgcgaagacctggggcctcagtgaaagt 154
    |||||||
DB 2 aggtgcagctgcagcagctctgggctgaactgcgaagacctggggcctcagtgaaagt 61
QY 155 cctgcgaagctctgcagcagctcttactgagtcacagcagctgggtgtaaaagagc 214
    |||||||
DB 62 cctgcgaagccttcgctgacaccttcacacagcagctggatgcactggctcagcagagc 121
QY 215 ctgcgaagctgcagcagctctggaatgagttgatacttaactcctagcctggtgatactaaata 274
    |||||||
DB 122 ctgcgacagagccttgagtgatgcagagctttatccacacagcagcggcctgactatcaca 181
QY 275 atcagaagctcagaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 334
    |||||||
DB 182 atcagaagctcagaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 241
QY 335 tgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 394
    |||||||
DB 242 tgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 301
QY 395 atgacatcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 448
    |||||||
DB 302 atgacatcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 361
QY 449 cagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 508
    |||||||
DB 362 cagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 421
QY 509 tgcctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 568
    |||||||
DB 422 agctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 481
QY 569 gcaagtcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 628
    |||||||
DB 482 gcaagtcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 541
QY 629 ccaagaagatgattatgacacatccaactgctctgagtcctgctcactcagcagcagcagcagcagc 688
    |||||||
DB 542 ccaagaagatgattatgacacatccaactgctctgagtcctgctcactcagcagcagcagcagcagc 601
QY 689 gcaagtcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 748
    |||||||
DB 602 gcaagtcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 661
QY 749 ccaactatcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 802
    |||||||
DB 662 ccaactatcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 721
QY 803 ccaagtcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 818
    |||||||
DB 722 ccaagtcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 737
```

```
RESULT 6
US-08-553-497A-25
; Sequence 25, Application US/08553497A
```

```
Patent No. 5844093
GENERAL INFORMATION:
APPLICANT: KETTERBROUGH, C. A.
APPLICANT: BENDIG, MARY M.
APPLICANT: ANSELL, KEITH H.
APPLICANT: GUSSEW, DETLEF
APPLICANT: ADAN, JAUME
APPLICANT: MITJANS, FRANCESCA
APPLICANT: ROSELL, ELISABET
APPLICANT: BLASCO, FRANCESC
APPLICANT: PILARIS, JAUME
TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD. SUITE 1400
CITY: ARLINGTON
STATE: VA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,497A
FILING DATE: 17-NOV-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/EP95/00978
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94104160.0
FILING DATE: 17-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94118970.6
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1726
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
INFORMATION FOR SEQ. ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 726 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHEetical: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: mouse
STRAIN: Balb/c
TISSUE TYPE: splenocytes
IMMEDIATE SOURCE:
CLONE: 5 F 1 (single-chain Fv, heavy, light chain,
FEATURE: linker)
NAME/KEY: CDS
LOCATION: 1..726
US-08-553-497A-25
```

```
Query Match      53.2%; Score 483.8; DB 2; Length 726;
Best Local Similarity 81.0%; Pred. No. 6.1e-140;
Matches 592; Conservative 0; Mismatches 127; Indels 12; Gaps 2;
```





Db	242	TGCAACTCAGCAGCGCTGACATCTGTAGGACCTGTGGGCTCTATTACTGTGCCAGTGGGACT	301
Oy	335	atgatactaacag-----ecttgactacttggggccaaggacacactctcaagctctct	448
Db	302	ATGATTACAGCGGACCGGTACTTTGACTACTGTGGGCCAAGGAGCCACGTCACCTCTCCT	361
Oy	449	cagcccaaacacacaccacagcttcaagaaggtgaattctcaagacacagcgtagatctg	508
Db	362	CAGGTGGCGGTGGCTCG-----GGCGTGGTGGGTCGGGTGGCGGGATCTGACATTG	415
Oy	509	tgctactcagctctccagaatcatatgtctgactctccagggaagaagtcacatgaact	568
Db	416	AGCTCACCACCTCTCCAGCATCATGTCTGTGCATCTCCAGGGGGAAGATGATCACCATGACT	475
Oy	559	gcagtgccagctcaagtgtaagtaactgaactgtgtccagccaagaatctaggcacctccc	628
Db	476	GCAGTCCACGCTCAGATGTATGATTACATGTACTGTGTGTCACCAACCAAAACCAGGATCTCC	533
Oy	629	ccaaaaagatgatatatatacacatccacaactcgtgtctctgagctccctctcaactcagg	688
Db	536	CCAGACTCCTGATTATATGACATCAATCCACCTCGGCTTCGGAGTCCCTGTTCGGCTTCAGTG	595
Oy	689	gcagtgagcttcgggaacctcttactctctcaaatccagcggatctgaagcctggaagatctg	748
Db	556	GCAGTGGGCTCTGGGACCTTACTCTCTCCAAATCAGCCGATGGAGGCTGAAGATCTCG	655
Oy	749	ccacttatacttcgcagcagtgtagtagtaacca-----ttcagtlctcgtctcggga	802
Db	656	CCACTTATTACTGCAGCAGGTGAGTAGTATCCACCCATGTACACGTTGGAGGGGGA	715
Oy	803	caagcttgaaataaa 818	
Db	716	CCAACTGGAATAAA_731	

US-08-553 497A-21  
: Sequence 21, Application US/08553497A  
: Patent No. 5844093  
: GENERAL INFORMATION:  
: APPLICANT: KETTELBOROUGH, C. A.  
: APPLICANT: BENDIG, MARY M.  
: APPLICANT: ANSELL, KEITH H.  
: APPLICANT: GUSSON, DETLEF  
: APPLICANT: ADAN, JAUME  
: APPLICANT: MITJANS, FRANCESC  
: APPLICANT: ROSELL, ELISABET  
: APPLICANT: BLASCO, FRANCESC  
: APPLICANT: PIULATS, JAUME  
: TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR  
: TITLE OF INVENTION: ANTIBODIES  
: NUMBER OF SEQUENCES: 30  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.  
: STREET: 2200 CLARENDON BLVD. SUITE 1400  
: CITY: ARLINGTON  
: STATE: VA  
: COUNTRY: US  
: ZIP: 22201  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Floppy disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: PatentIn Release #1.0, Version #1.30  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/08/553,497A  
: FILING DATE: 17-NOV-1995  
: CLASSIFICATION: 530  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: WO PCT/EP95/00978  
: FILING DATE: 16-MAR-1995  
: PRIOR APPLICATION DATA: EP 94104160.0

1 FILING DATE: 17-MAR-1994  
 2 PRIOR APPLICATION DATA:  
 3 APPLICATION NUMBER: EP 94118970.6  
 4 FILING DATE: 02-DEC-1994  
 5 ATTORNEY/AGENT INFORMATION:  
 6 NAME: HAMLET-KING, DIANA  
 7 REGISTRATION NUMBER: 33,302  
 8 REFERENCE/DOCKET NUMBER: MERCK 1726  
 9 TELECOMMUNICATION INFORMATION:  
 10 TELEPHONE: 703-243-6333  
 11 TELEFAX: 703-243-6410  
 12 INFORMATION FOR SEQ ID NO: 21:  
 13 SEQUENCE CHARACTERISTICS:  
 14 LENGTH: 732 base pairs  
 15 TYPE: nucleic acid  
 16 STRANDEDNESS: single  
 17 TOPOLOGY: linear  
 18 MOLECULE TYPE: cDNA  
 19 HYPOTHETICAL: NO  
 20 ANTI-SENSE: NO  
 21 FRAGMENT TYPE: N-terminal  
 22 ORIGINAL SOURCE:  
 23 ORGANISM: mouse  
 24 STRAIN: Balb/c  
 25 TISSUE TYPE: splenocytes  
 26 IMMEDIATE SOURCE:  
 27 CLONE: 3 D 3 (single-chain Fv, heavy and light chain  
 28 CLONE: plus linker)  
 29 FEATURE:  
 30 NAME/KEY: CDS  
 31 LOCATION: 1..732  
 32 US-08-553-497A-21

Query Match	Similarity	Score	471.6:	DB 2:	Length	732:
Best Local	Similarity	80.7%:	Pred. No. 3.6e-136:			
Matches	594:	Conservative	0:	Mismatches	124:	Indels
						Gaps
						3







Db 316 ctctgcagcagctgcctatttgcagatcaacaacactccaataaataatgaggacaacggtataca 375  
 Oy 375 ttactgtgcagaatataatgatgatcaattacaagccttgactactcggggccaagggaccac 433  
 Db 376 ttctgtgtctaggggcggt-----agccttgactactcggggccaagggaccac 422  
 Oy 435 tctcaacgtctccccaagccaacaacaacccaagccttgaagaagtgtaatttcagagc 494  
 Db 424 tctcaacgtctccccaag-----gtgaaggcggttcaggcggaagtggcagcgcggttg 477  
 Oy 495 aagcgatagatcgtgtgtcaactcagctccagcaatcatgtctgcattccaaggaggaa 554  
 Db 478 cgagatcgcgaatgtgttccaccagctccagatattcatgtctgcattccaaggaggaa 537  
 Oy 555 ggttaacctatgcctgcagtgccagctcaactcaagtgttaagttaactatgtaactcgtgtaccagaa 614  
 Db 538 ggttaacctatgcctgcagtgccagctcaactcaagtgttaagttaactatgtaactcgtgtaccagaa 597  
 Oy 615 gtcaagcaccctccccaagaatgatattatgatacatccaactctgtgtgagctcc 674  
 Db 558 gccaagatccctccccaagaccctccgattcaatgccaatccaactgctcttgagctcc 655  
 Oy 675 tgtcaactcaggggcagtggtgtctggagccttactctctcaactcagcggcatgaa 734  
 Db 658 tgttgcctcagtggtgggtgtgtctggagccttactctctcaactcagcggcatgaa 717  
 Oy 725 ggtcgaagaatcgtccacttactctccagcagtggaatgaatccatccaactgctcg 794  
 Db 718 ggtcgaagaatcgtccacttactctccagcagtggaatgaatccaactgctcg 777  
 Oy 795 ctctggggccaagtttgaataaacggtgc-----tgatactgcaccaactgatac 845  
 Db 778 tggaggccaccaagctgtgaatcatcagcggccgcatcatcatccatccacgagggcgcc 837  
 Oy 846 cgaacaaagctgtatctcagaagaagacctaa 878  
 Db 838 agaacaaaactcatctcagaagaagatctgaa 870

RESULT 13  
 US-08-800-198-7  
 Sequence 7, Application US/08800198  
 Patent No. 5942602  
 GENERAL INFORMATION:  
 APPLICANT: WELS, WINFRIED S.  
 APPLICANT: SCHMIDT, MATTHIAS  
 APPLICANT: VAKALOPOULOU, EVANGELIA  
 APPLICANT: SCHNEIDER, DOUGLAS  
 TITLE OF INVENTION: GROWTH FACTOR RECEPTOR ANTIBODIES  
 NUMBER OF SEQUENCES: 17  
 CORRESPONDENCE ADDRESSES:  
 ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.  
 STREET: 2200 CLARENDON BLVD, SUITE 1400  
 CITY: ARLINGTON  
 STATE: VA  
 COUNTRY: US  
 ZIP: 22201  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/800,198  
 FILING DATE: 13-FEB-1997  
 CLASSIFICATION: 530  
 ATTORNEY/AGENT INFORMATION:  
 NAME: HAMLET-KING, DIANA  
 REGISTRATION NUMBER: 33,302  
 REFERENCE/DOCKET NUMBER: SCH 1576  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 703-243-6333

```

: TELEFAX: 703-243-6410
: INFORMATION FOR SEQ ID NO: 7:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 720 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: other nucleic acid
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: US-08-800-198-7

```

Query Match	41.8%;	Score 379.8;	DB 2;	Length 720;
Best Local Similarity	72.3%;	Pred. No. 7.8e-108;		
Matches 524;	Conservative 0;	Mismatches 192;	Indels 9;	Gaps 2;

QY	94	caggctgcagcgcagcagctctcgaggccgaactgcgaagccttgaggcctcagtgaaagt	153
Db	1	CAAGTCAGCTGCAGGAGATCTGGGGGCTGMACTGGCAAAACCTGGGGGCTCATGTGAATG	60
QY	154	tccctcgaaggtctctggtctaaccttactagtagtacacgatactgacttggtaaacagaag	213
Db	61	TCCTGCAAGGCTTCTGGGTACTACCTTACTAATCACTGATGACACTGGTGACAGAGG	120
QY	214	ccctgcgaaggtctcggaaatggaatggaatacattatcctcagccgttgtaactaatlac	273
Db	121	CCTGGACAGGCTGCTGATGATGATTGGATACACTAATCTAACCTGGTTTACTGATTTTC	180
QY	274	aatagaagtccaaggagcaagagccaaacttactccagacaaatctctccacagaagctac	333
Db	181	AATCAGAGTTTCAAGAGCAAMGGCCACTGTGCTGCAACAAATCTCTCCACACAGCTTAC	240
QY	334	atgcaactgcagcagccgcgcacactcgcgaagactctgcagctcatctactctgtaagatat	393
Db	241	ATGCACACTGACAGCGGCTGACACTGTGAAGACTCTGCATTTACTTACTGTGCAAGAGGGAT	300
QY	394	gattatcaattacagcgttgaactacttggggccaaagcaccactcacaagctcctcaagcc	453
Db	301	TACTACGGCTACGACTTGGTTACTGCTGAGGCGCAAGGACACAGGTCACCGTTCTCTGGC	360
QY	454	aaaacaacaccacaagcttgaagaagtgaaatlttcagaagcagcgtagatctcgtgtc	513
Db	361	GGTGGCGGTTT-----TGGTGGGGGTGGCTCCGGCGGTGGCTTGCATTCACGCTG	414
QY	514	actcagctctccagcaatcatctctgcacatcccaaggaggaagtcaacatgcagctcagt	573
Db	415	ACCCAGTCTCCAGGCATCTCTCTGTGAAGTCACAGGAAGAAAGTCATTTCTCTCGAGG	474
QY	574	gccacgtcaag--tgtaagttacatgaactgtaactgtaaccagaagaagtcaggacctcccc	630
Db	475	GCCAGTCAGACATTTGGCACAAATATACACGTGATCAGCAAGAAACAAATGGTTCTTCCA	534
QY	631	aaaagaatggaatttatgacacatcccaactcgtctcttgagttccctcgtcaactccaagggc	690
Db	535	AGGCTTCTCATAAAGTATGCTTCTGATGCTATCTCTGGGATCCCTTCCAGAGTTAATGGG	594
QY	691	agtgtgctcgtggaaccttactcctctcaaatcagcggcagtgaagctgtcgc	750
Db	595	AGTGGATCAGGGACAGATTTTACTCTTAAGCATCAACAGTGTGGAGTCTGCAAGATATTGCA	654
QY	751	actatactactgcagcagctggagtagtaaacccaacttcaacgttctcgtctcgtggagcaagt	810
Db	655	GATTATTTACTCTCAACAAAGTATAGTGTGCCAACACGTTCCGTCGTGGAGCAAAAGCTC	714
QY	811	gaat 815	
Db	715	GAGAT 719	

RESULT 14  
US-09-296-595-7  
; Sequence 7, Application US/09296595A



D	134	CCAGTATTGGATGCACGTGGGTGAAAGCAAGAGCGCTGGACAAGCGCTTGAGTGGATTGGAG	253
OY	242	acattaatcctgaacccguygttatacctaattaaatcagaagttcagaagacagccacat	301
D	254	AGATTAAATCCTACCAACGCGTGTCTATTATTCAAATGGAAGTTCCAAAGCAAGGCCAC	313
OY	302	tgaatacagagaanaatccctccagacagccttaacatgaaactgagagagcctgaactgag	361
D	314	TGACTGTGAGACAAATCTTCCACGTCACAGCTTCATGCAAGCTCAGCGCTACATCTGAGG	373
OY	362	actctgcagttctattactgtgcaagataatatagtatgatalcatlaacgcttgaactgag	421
D	374	ACTCGCGCGTATTACTGTGTCAAGACGGTATG-----GTAACTCCTTTGACACTGGG	427
OY	422	gccaaagacacacactcactcagttccctccagccaaacaaacacaccccaagctgaagaag	481
D	428	GCCAAAGGACCAACGCTCACCGTCTCTCCAGCAATGATGATAA-----	468
OY	482	aatttcagaagacacgcgctgaatatactgctcactcactgactcaccagaatcatgtcga	541
D	469	-----AGGGACATCGAGCTCACACCAGTCTCCAGATTCTTTGGCTGTGT	511
OY	542	ctccagggggaagaagttcaaccatgacctgcagttccagctcaagtga-----	568
D	512	CTTAAAGGCAAGAGGCCACCATATCTCCGACAGGCACTGAAGCTTGATAGTTATGGCA	571
OY	589	-agttacatgtaactgctgataccagcagaagtaagcactcccccnaaagaatgattatg	646
D	572	ATAGTTTATATGCACTGTGTACCAAGCAAGAAACCAAGACAGCAACCCAACTCCTATATC	631
OY	647	acaacatccaacatgctcttgcagttccctgtcactcattcagggcagtgagttcgcagct	706
D	632	GTGCTATCCCAACCTTGAAATCTTGCGATTTCTTGCCAGAGTTCAGTGGCACATGGGCTT	691
OY	707	cttaactcttcaacatacagcgagcagtaaggtctgaagttgttcgaactataactgcagc	766
D	682	ACTTCAACCTTACCACTTATATCTGTGGAGGCTGATGTGTAACCTATTATTTGTCAAC	751
OY	767	agtg-----gagtagtaaacccatcactcgtctcgcgtcgggacaaagttggaataaac	820
D	752	AAAGATGATGATATCCGATCATGTACACGTTGGAGGGGGGACCAACCTCGAGATCAAC	811
OY	821	ggg 823	
D	812	ggg 814	

**THIS PAGE BLANK (USPTO)**